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Term: L1 same (acidothermus cellulolyticus)

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Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ			
L7	L5 same exoglucanase	2	L7
L6	L5 same (family 48)	0	L6
L5	L1 same (acidothermus cellulolyticus)	22	L5
L4	L1 same (glycoside hydrolase)	38	L4
L3	L1 same (GH48 or family 48 or Gux1)	0	L3
L2	L1 same (GH48 or family 48 or Gux1)	0	L2
L1	cellulase	8139	L1

END OF SEARCH HISTORY

L5: Entry 7 of 22 File: USPT Nov 9, 1999

DOCUMENT-IDENTIFIER: US 5981835 A
TITLE: Transgenic plants as an alternative source of lignocellulosic-degrading enzymes

Detailed Description Text (243):
Tucker et al. (1989), Ultra-thermostable cellulases from Acidothermus cellulolyticus comparison of temperature optima with previously reported cellulases. Biotechnology 7:817-820.

Other Reference Publication (30):
Tucker et al. (1989), Ultra-thermostable cellulases from Acidothermus cellulolyticus comparison of temperature optima with previously reported cellulases. Biotechnology 7:817-820.

=> d his

(FILE 'HOME' ENTERED AT 08:40:02 ON 12 FEB 2003)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 08:40:13 ON 12 FEB 2003

SEA (GLYCOSIDE HYDROLASE) OR (GLYCOSYL HYDROLASE)

1326	FILE AGRICOLA
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29	FILE CEABA-VTB
12	FILE CONFSCI
1	FILE CROPB
1	FILE CROPU
4909	FILE DDFB
3	FILE DDFU
384	FILE DGENE
4909	FILE DRUGB
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10631	FILE MEDLINE
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7	FILE OCEAN
215	FILE PASCAL
1	FILE PHAR
2	FILE PROMT
968	FILE SCISEARCH
1170	FILE TOXCENTER
292	FILE USPATFULL
5	FILE USPAT2
169	FILE VETB
56	FILE WPIDS
56	FILE WPINDEX

L1 QUE (GLYCOSIDE HYDROLASE) OR (GLYCOSYL HYDROLASE)

FILE 'JICST-EPLUS, MEDLINE, DRUGB, CABA, AGRICOLA, TOXCENTER, SCISEARCH, CAPLUS, BIOSIS' ENTERED AT 08:42:11 ON 12 FEB 2003

L2 0 S L1 AND (GH48) OR (GUX1)
L3 51 S L1 AND (FAMILY 48)
L4 4 S L3 AND (ACIDOTHERMUS OR CELLULOLYTICUS)
L5 0 S L1 AND (GH48 OR GUX1)

L6	1	DUP REM L4 (3 DUPLICATES REMOVED)
L7	13	DUP REM L3 (38 DUPLICATES REMOVED)
L8	45712	S CELLULASE
L9	49	S L8 AND (FAMILY 48 OR GH48)
L10	110	S L8 AND (ACIDOTHERMUS CELLULOLYTICUS)
L11	0	S L10 AND (FAMILY 48 OR GH48 OR GUX1)
L12	16	S L10 AND (EXOGLUCANASE OR CBD)
L13	4	DUP REM L12 (12 DUPLICATES REMOVED)
L14	17	DUP REM L9 (32 DUPLICATES REMOVED)

=> d l13 ibib ab 1-4

L13 ANSWER 1 OF 4 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 1998290861 MEDLINE
DOCUMENT NUMBER: 98290861 PubMed ID: 9627391
TITLE: Hydrolysis of cellulose using ternary mixtures of purified **cellulases**.
AUTHOR: Baker J O; Ehrman C I; Adney W S; Thomas S R; Himmel M E
CORPORATE SOURCE: Biotechnology Center for Fuels and Chemicals, National Renewable Energy Laboratory, Golden, CO 8040, USA.
SOURCE: APPLIED BIOCHEMISTRY AND BIOTECHNOLOGY, (1998 Spring) 70-72 395-403.
Journal code: 8208561. ISSN: 0273-2289.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980903
Last Updated on STN: 19980903
Entered Medline: 19980824

AB The saccharification of microcrystalline cellulose by reconstituted ternary mixtures of purified **cellulases** (one endoglucanase and two cellobiohydrolases) has been studied over the entire range of mixture compositions. Ternary plots are used to compare the performance of five synthetic mixtures drawn from the **cellulase** systems of **Acidothermus cellulolyticus**, Trichoderma reesei, Thermomonospora fusca, and Thermotoga neapolitana. Results reveal that at least one synthetic mixture utilizing enzymes from three different organisms delivers performance competitive with that of a "native" (i.e., co-evolved) ternary system drawn exclusively from T. reesei. This heterologous system, consisting of the endoglucanase E1 from A. cellulolyticus and the **exoglucanases** CBHI from T. reesei and E3 from T. fusca, is forgiving from the system-design point of view, in that it delivers high saccharification rates over a wide range of mixture compositions.

L13 ANSWER 2 OF 4 AGRICOLA DUPLICATE 2
ACCESSION NUMBER: 96:12124 AGRICOLA
DOCUMENT NUMBER: IND20499125
TITLE: Quantitation of **Acidothermus cellulolyticus** E1 endoglucanase and Thermomonospora fusca E3 **exoglucanase** using enzyme-linked immunosorbent assay (ELISA).
AUTHOR(S): Nieves, R.A.; Chou, Y.C.; Himmel, M.E.; Thomas, S.R.
CORPORATE SOURCE: National Renewable Energy Laboratory, Golden, CO.
AVAILABILITY: DNAL (QD415.A1J62)
SOURCE: Applied biochemistry and biotechnology, Spring 1995. Vol. 51/52 p. 211-223
Publisher: Totowa, N.J. : Humana Press.
CODEN: ABIBDL; ISSN: 0273-2289
NOTE: Paper presented at the Sixteenth Symposium on Biotechnology for Fuels and Chemicals, May 9-13, 1994, Gatlinburg, Tennessee.
Includes references
PUB. COUNTRY: New Jersey; United States
DOCUMENT TYPE: Article
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English

AB Two distinct quantitative indirect ELISAs were developed to determine the concentration of recombinant **cellulase** enzymes in culture filtrates. A monoclonal antibody (E1P7) was used as the primary antibody in developing an ELISA specific for **Acidothermus**

cellulolyticus E1 endoglucanase. Likewise, a polyclonal rabbit serum (Ab684) was used to develop an ELISA specific for Thermomonospora fusca E3 **exoglucanase**. Dose-response curves indicated a dynamic range for both assays between 0.01 and 0.08 micrograms/mL (1-8 ng/assay) when purified enzymes were used as standards. These assays have been used to estimate concentrations of secreted recombinant E1 and/or E3 in culture supernatants of Streptomyces lividans strain TK24 in which the corresponding genes have been cloned and expressed.

L13 ANSWER 3 OF 4 SCISEARCH COPYRIGHT 2003 ISI (R) DUPLICATE 3
ACCESSION NUMBER: 96:111961 SCISEARCH
THE GENUINE ARTICLE: BE51K
TITLE: SYNERGISM BETWEEN PURIFIED BACTERIAL AND FUNGAL **CELLULASES**
AUTHOR: BAKER J O (Reprint); ADNEY W S; THOMAS S R; NIEVES R A; CHOU Y C; VINZANT T B; TUCKER M P; LAYMON R A; HIMMEL M E
CORPORATE SOURCE: NATL RENEWABLE ENERGY LAB, DIV ALTERNAT FUEL, APPLIED BIOL SCI BRANCH, 1617 COLE BLVD, GOLDEN, CO, 80401 (Reprint)
COUNTRY OF AUTHOR: USA
SOURCE: ACS SYMPOSIUM SERIES, (1995) Vol. 618, pp. 113-141. ISSN: 0097-6156.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: ENGLISH
REFERENCE COUNT: 59
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A standardized comparative study measured glucose release and synergistic effects in the solubilization of microcrystalline cellulose by binary mixtures of 11 fungal and bacterial **cellulases** (eight endoglucanases and three **exoglucanases**). Evaluation of 16 endo/exo pairs revealed that bacterial/fungal hybrid pairs are very effective in solubilizing microcrystalline cellulose. Of nine bacterial/fungal hybrid pairs studied, six were ranked among the nine most synergistic combinations, and six bacterial/fungal pairs were also among the top nine pairs in terms of soluble-sugar release. One hybrid pair (**Acidothermus cellulolyticus** E1 and Trichoderma reesei CBH I) was ranked first in both synergism and sugar-release. In exo/exo synergism experiments, the performance of Thermomonaspora fusca E(3) confirmed its mode of action as ''CBH II-like'' (i.e., E(3) is synergistic with T. reesei CBH I but not with T. reesei CBH II). Studies of endo/endo interactions suggested a possible means of categorizing endoglucanases in terms of substrate specificity.

L13 ANSWER 4 OF 4 CABA COPYRIGHT 2003 CABI DUPLICATE 4
ACCESSION NUMBER: 95:102060 CABA
DOCUMENT NUMBER: 950308088
TITLE: A new thermostable endoglucanase, **Acidothermus cellulolyticus** E1. Synergism with Trichoderma reesei CBH I and comparison to Thermomonospora fusca E5
AUTHOR: Baker, J. O.; Adney, W. S.; Nieves, R. A.; Thomas, S. R.; Wilson, D. B.; Himmel, M. E.
CORPORATE SOURCE: Alternative Fuels Division, National Renewable Energy Laboratory, 1617 Cole Blvd., Golden, CO 80401, USA.
SOURCE: Applied Biochemistry and Biotechnology. Part A, Enzyme Engineering and Biotechnology, (1994) Vol. 45/46, pp. 245-256. 19 ref.
Meeting Info.: Proceedings of the fifteenth symposium on biotechnology for fuels and chemicals, held at Colorado Springs, USA, 10-14 May 1993.
DOCUMENT TYPE: Conference Article; Journal
LANGUAGE: English

AB A new thermostable endoglucanase (**Acidothermus cellulolyticus** E1) and another bacterial endoglucanase

(Thermomonospora fusca E5) each exhibit striking synergism with a fungal cellobiohydrolase (Trichoderma reesei CBH I [a cellulose 1,4- beta -cellulobiosidase]) in the saccharification of microcrystalline cellulose. In neither case did the endoglucanase:**exoglucanase** ratio that demonstrated maximum synergism coincide exactly with the ratio that actually released the maximum quantity of soluble sugar for a given total **cellulase** loading. The difference between the two ratios, after significant hydrolysis of the substrate, was considerably larger in the case of A. cellulolyticus E1. For both endoglucanase pairings with CBH I, the offset between the ratio for maximum synergism and the ratio for maximum soluble sugar production was found to be a function of digestion time.

=> d l14 ibib ab 1-17

L14 ANSWER 1 OF 17 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002354510 MEDLINE
DOCUMENT NUMBER: 22092324 PubMed ID: 12096911
TITLE: The crystal structure and catalytic mechanism of cellobiohydrolase CelS, the major enzymatic component of the Clostridium thermocellum Cellulosome.
AUTHOR: Guimaraes Beatriz G; Souchon Helene; Lytle Betsy L; David Wu J H; Alzari Pedro M
CORPORATE SOURCE: Unite de Biochimie Structurale, CNRS URA 2185, Institut Pasteur, 25 rue du Dr. Roux, 75724 Paris cedex 15, France.
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (2002 Jul 12) 320 (3) 587-96. Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: PDB-1L1Y; PDB-1L2A
ENTRY MONTH: 200208
ENTRY DATE: Entered STN: 20020707
Last Updated on STN: 20020816
Entered Medline: 20020815

AB Cellobiohydrolase CelS plays an important role in the cellulosome, an active **cellulase** system produced by the thermophilic anaerobe Clostridium thermocellum. The structures of the catalytic domain of CelS in complex with substrate (cellohexaose) and product (cellobiose) were determined at 2.5 and 2.4 A resolution, respectively. The protein folds into an (alpha/alpha)(6) barrel with a tunnel-shaped substrate-binding region. The conformation of the loops defining the tunnel is intrinsically stable in the absence of substrate, suggesting a model to account for the processive mode of action of **family 48** cellobiohydrolases. Structural comparisons with other (alpha/alpha)(6) barrel glycosidases indicate that CelS and endoglucanase CelA, a sequence-unrelated family 8 glycosidase with a groove-shaped substrate-binding region, use the same catalytic machinery to hydrolyze the glycosidic linkage, despite a low sequence similarity and a different endo/exo mode of action. A remarkable feature of the mechanism is the absence, from CelS, of a carboxylic group acting as the base catalyst. The nearly identical arrangement of substrate and functionally important residues in the two active sites strongly suggests an evolutionary relationship between the cellobiohydrolase and endoglucanase families, which can therefore be classified into a new clan of glycoside hydrolases. (c) 2002 Elsevier Science Ltd.

L14 ANSWER 2 OF 17 SCISEARCH COPYRIGHT 2003 ISI (R) DUPLICATE 2
ACCESSION NUMBER: 2003:30883 SCISEARCH
THE GENUINE ARTICLE: 626VV
TITLE: The major component of the cellulosomes of anaerobic fungi from the genus Piromyces is a **family 48** glycoside hydrolase
AUTHOR: Steenbakkers P J M; Freelove A; van Cranenbroek B; Sweegers B M C; Harhangi H R; Vogels G D; Hazlewood G P; Gilbert H J; den Camp H J M O (Reprint)
CORPORATE SOURCE: Univ Nijmegen, Fac Sci, Dept Microbiol, Toernooiveld 1, NL-6525 ED Nijmegen, Netherlands (Reprint); Univ Nijmegen, Fac Sci, Dept Microbiol, NL-6525 ED Nijmegen, Netherlands; Babraham Inst, Lab Mol Enzymol, Cambridge CB2 4AT, England; Univ Newcastle Upon Tyne, Dept Biol & Nutr Sci, Newcastle Upon Tyne NE1 7RU, Tyne & Wear, England
COUNTRY OF AUTHOR: Netherlands; England
SOURCE: DNA SEQUENCE, (JAN 2002) Vol. 13, No. 6, pp. 313-320. Publisher: TAYLOR & FRANCIS LTD, 4 PARK SQUARE, MILTON PARK,, ABINGDON OX14 4RN, OXON, ENGLAND.

ISSN: 1042-5179.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 45
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Sequencing of two cDNAs from the anaerobic fungi Piromyces equi and Piromyces sp. strain E2 revealed that they both encode a glycoside hydrolase (GH) **family 48 cellulase**, containing two C-terminal fungal dockerin domains. N-terminal sequencing of the major component of the Piromyces multi-enzyme **cellulase** /hemicellulase complex, termed the cellulosome, showed that these 80 kDa proteins corresponded to the GH **family 48** enzyme. These data show for the first time that GH **family 48** **cellulases** are not confined to bacteria, and that bacterial and fungal cellulosomes share the same pivotal component.

L14 ANSWER 3 OF 17 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002161351 IN-PROCESS
DOCUMENT NUMBER: 21889743 PubMed ID: 11893054
TITLE: The Clostridium cellulovorans cellulosome: an enzyme complex with plant cell wall degrading activity.
AUTHOR: Doi R H; Tamaru Y
CORPORATE SOURCE: Section of Molecular & Cellular Biology, Division of Biological Sciences, University of California, Davis 95616, USA.. rhdoi@ucdavis.edu
SOURCE: Chem Rec, (2001) 1 (1) 24-32. Ref: 33
Journal code: 101085550. ISSN: 1527-8999.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020315
Last Updated on STN: 20021211

AB Cellulose comprises a major portion of biomass on the earth, and the turnover of this material contributes to the CO2 cycle. **Cellulases** , which play a major role in the turnover of cellulosic materials, have been found either as free enzymes that work synergistically, or as an enzyme complex called the cellulosome. This review summarizes some of the general properties of cellulosomes, and more specifically, the properties of the Clostridium cellulovorans cellulosome. The C cellulovorans cellulosome is an extracellular enzyme complex with a molecular weight of about 1 x 10(6), and is comprised of at least ten subunits. The major subunit is the scaffolding protein CbpA, with a molecular weight of 189,000. This nonenzymatic subunit contains a cellulose binding domain (CBD) that binds the cellulosome to the substrate, nine conserved cohesins or enzyme binding domains, and four conserved surface layer homologous (SLH) domains. It is postulated that the SLH domains help to bind the cellulosome to the cell surface. The cellulosomal enzymes include **cellulases** (family 5 and 9 endoglucanases and a **family** **48** exoglucanase), a mannanase, a xylanase, and a pectate lyase. The cellulosome is capable of converting Arabidopsis and tobacco plant cells to protoplasts. One of the endoglucanases, EngE, contains three tandemly repeated SLHs at its N-terminus, and therefore appears capable of binding to the scaffolding protein CbpA as well as to the cell surface. Cellulosomes can attack crystalline cellulose, but the free cellulosomal enzymes can attack only soluble and amorphous celluloses. Nine genes for the cellulosome are found in a gene cluster cbpA-exgS-engH-engK-hbpA-engL-manA-engM-engN. Other cellulosomal genes such as engB, engE, and engY are not linked to the major gene cluster or to each other. By determining the structure and function of the cellulosome, we hope to increase the efficiency of the cellulosome by genetic engineering techniques.

L14 ANSWER 4 OF 17 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2001086784 MEDLINE
DOCUMENT NUMBER: 20558242 PubMed ID: 11106416
TITLE: Temporal secretion of a multicellulolytic system in Myxobacter sp. AL-1. Molecular cloning and heterologous expression of cel9 encoding a modular endocellulase clustered in an operon with cel48, an exocellobiohydrolase gene.
AUTHOR: Avitia C I; Castellanos-Juarez F X; Sanchez E; Tellez-Valencia A; Fajardo-Cavazos P; Nicholson W L; Pedraza-Reyes M
CORPORATE SOURCE: Institute of Investigation in Experimental Biology, Faculty of Chemistry, University of Guanajuato, Mexico.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2000 Dec) 267 (24) 7058-64.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010118

AB The Gram-negative soil micro-organism Myxobacter sp. AL-1 possesses at least five extracellular **cellulases**, the production of which is regulated by the growth cycle. We cloned the complete gene for one of these **cellulases**, termed cel9, which encoded a 67-kDa modular family 9 endoglycohydrolase, which was produced during the stationary phase of growth and was strongly enhanced by avicel. The predicted product of cel9 matches the structural architecture of family 9 **cellulases** such as Thermonospora fusca endo/exocellulase E4. Cel9 protein was synthesized in Escherichia coli from a multicopy plasmid and in Bacillus subtilis from the isopropyl thiogalactoside-inducible Pspac promoter and was purified from the culture medium. Thermal stability, optimum pH and temperature dependence of Cel9 were similar when expressed from either source, and were indistinguishable from related **cellulases** produced by thermophilic bacteria. Downstream from cel9 was found a partial ORF, designated cel48, the deduced product of which was highly similar to bacterial exocellobiohydrolases and processive endoglucanases belonging to **family 48** of the glycosyl hydrolases. The cel9 and cel48 genes appear to be arranged as part of an operon.

L14 ANSWER 5 OF 17 MEDLINE
ACCESSION NUMBER: 2000495112 MEDLINE
DOCUMENT NUMBER: 20389519 PubMed ID: 10931180
TITLE: Cloning, expression and characterization of a **family 48** exocellulase, Cel48A, from Thermobifida fusca.
AUTHOR: Irwin D C; Zhang S; Wilson D B
CORPORATE SOURCE: Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY, USA.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2000 Aug) 267 (16) 4988-97.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20021210
Entered Medline: 20001018

AB The gene for a 104-kDa exocellulase, Cel48A, formerly E6, was cloned from

Thermobifida fusca into Escherichia coli and Streptomyces lividans. The DNA sequence revealed a type II cellulose-binding domain at the N-terminus, followed by a FNIII-like domain and ending with a glycosyl hydrolase **Family 48** catalytic domain. The enzyme and catalytic domain alone were each expressed in and purified from S. lividans and had very low catalytic activity on swollen cellulose, carboxymethyl cellulose, bacterial microcrystalline cellulose and filter paper. However, in synergistic assays on filter paper, the addition of Cel48A to a balanced mixture of T. fusca endocellulase and exocellulase increased the specific activity from 7.9 to 11.7 micromol cellobiose.min-1.mL-1, more than 15-fold higher than any single enzyme alone. Cel48A retained > 50% of its maximum activity from pH 5 to 9 and from 40 to 60 degrees C. Using SWISSMODEL, the amino-acid sequence of the Cel48Acd was modeled to the known structure of Clostridium cellulolyticum CelF. **Family 48** enzymes are remarkably homologous at 35% identity for all their catalytic domains and some of the properties of the 10 members are discussed.

L14 ANSWER 6 OF 17 MEDLINE
ACCESSION NUMBER: 2000437099 MEDLINE
DOCUMENT NUMBER: 20398177 PubMed ID: 10940036
TITLE: A scaffoldin of the Bacteroides cellulosolvens cellulosome that contains 11 type II cohesins.
AUTHOR: Ding S Y; Bayer E A; Steiner D; Shoham Y; Lamed R
CORPORATE SOURCE: Department of Biological Chemistry, The Weizmann Institute of Science, Rehovot, Israel.
SOURCE: JOURNAL OF BACTERIOLOGY, (2000 Sep) 182 (17) 4915-25. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF224509
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20000928
Last Updated on STN: 20000928
Entered Medline: 20000921

AB A cellulosomal scaffoldin gene, termed cipBc, was identified and sequenced from the mesophilic cellulolytic anaerobe Bacteroides cellulosolvens. The gene encodes a 2,292-residue polypeptide (excluding the signal sequence) with a calculated molecular weight of 242,437. CipBc contains an N-terminal signal peptide, 11 type II cohesin domains, an internal family III cellulose-binding domain (CBD), and a C-terminal dockerin domain. Its CBD belongs to family IIIb, like that of CipV from Acetivibrio cellulolyticus but unlike the family IIIa CBDs of other clostridial scaffoldins. In contrast to all other scaffoldins thus far described, CipBc lacks a hydrophilic domain or domain X of unknown function. The singularity of CipBc, however, lies in its numerous type II cohesin domains, all of which are very similar in sequence. One of the latter cohesin domains was expressed, and the expressed protein interacted selectively with cellulosomal enzymes, one of which was identified as a **family 48** glycosyl hydrolase on the basis of partial sequence alignment. By definition, the dockerins, carried by the cellulosomal enzymes of this species, would be considered to be type II. This is the first example of authentic type II cohesins that are confirmed components of a cellulosomal scaffoldin subunit rather than a cell surface anchoring component. The results attest to the emerging diversity of cellulosomes and their component sequences in nature.

L14 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:327676 CAPLUS
TITLE: Attack of cellulose microcrystals by bacterial cellobiohydrolases.
AUTHOR(S): Gilkes, Neil R.; Imai, Tomoya; Kilburn, Doug; Warren,

Tony; Sugiyama, Junji
CORPORATE SOURCE: Department of Microbiology and Immunology, University of British Columbia, Vancouver, BC, V6T 1Z3, Can.
SOURCE: Book of Abstracts, 219th ACS National Meeting, San Francisco, CA, March 26-30, 2000 (2000), BTEC-057. American Chemical Society: Washington, D. C.
CODEN: 69CLAC
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB **Cellulase** systems from aerobic bacteria and fungi contain similar cellobiohydrolases exoglucanases that remove cellobiosyl residues from the ends of substrate mols. Related cellobiohydrolases from glucosyl hydrolase family 6 are found in both bacteria and fungi and attack substrates from the non-reducing end. Fungal cellobiohydrolases from family 7 and bacterial cellobiohydrolases from **family 48** belong to different enzyme families but both attack from the reducing end. The directions of attack by Cellulomonas fimi cellobiohydrolases CbhA and CbhB.

L14 ANSWER 8 OF 17 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 1998429479 MEDLINE
DOCUMENT NUMBER: 98429479 PubMed ID: 9755156
TITLE: The crystal structure of the processive endocellulase CelF of Clostridium cellulolyticum in complex with a thiooligosaccharide inhibitor at 2.0 A resolution.
AUTHOR: Parsiegla G; Juy M; Reverbel-Leroy C; Tardif C; Belaich J P; Driguez H; Haser R
CORPORATE SOURCE: Laboratoire d'Architecture et Fonction des Macromolecules Biologiques, Institut de Biologie Structurale et Microbiologie, Centre National de la Recherche Scientifique, Marseille cedex 20, France.
SOURCE: EMBO JOURNAL, (1998 Oct 1) 17 (19) 5551-62.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: PDB-1FCE
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981123
AB The mesophilic bacterium Clostridium cellulolyticum exports multienzyme complexes called cellulosomes to digest cellulose. One of the three major components of the cellulosome is the processive endocellulase CelF. The crystal structure of the catalytic domain of CelF in complex with two molecules of a thiooligosaccharide inhibitor was determined at 2.0 A resolution. This is the first three-dimensional structure to be solved of a member of the **family 48** glycosyl hydrolases. The structure consists of an (alpha alpha)6-helix barrel with long loops on the N-terminal side of the inner helices, which form a tunnel, and an open cleft region covering one side of the barrel. One inhibitor molecule is enclosed in the tunnel, the other exposed in the open cleft. The active centre is located in a depression at the junction of the cleft and tunnel regions. Glu55 is the proposed proton donor in the cleavage reaction, while the corresponding base is proposed to be either Glu44 or Asp230. The orientation of the reducing ends of the inhibitor molecules together with the chain translation through the tunnel in the direction of the active centre indicates that CelF cleaves processively cellobiose from the reducing to the non-reducing end of the cellulose chain.

L14 ANSWER 9 OF 17 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 1998361925 MEDLINE
DOCUMENT NUMBER: 98361925 PubMed ID: 9696784

TITLE: Cloning and DNA sequencing of the genes encoding Clostridium josui scaffolding protein CipA and **cellulase** CelD and identification of their gene products as major components of the cellulosome.
AUTHOR: Kakiuchi M; Isui A; Suzuki K; Fujino T; Fujino E; Kimura T; Karita S; Sakka K; Ohmiya K
CORPORATE SOURCE: Faculty of Bioresources, Mie University, Tsu 514, Japan.
SOURCE: JOURNAL OF BACTERIOLOGY, (1998 Aug) 180 (16) 4303-8. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB004845; GENBANK-AB011057
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19980917
Last Updated on STN: 20000303
Entered Medline: 19980904

AB The Clostridium josui cipA and celD genes, encoding a scaffolding-like protein (CipA) and a putative **cellulase** (CelD), respectively, have been cloned and sequenced. CipA, with an estimated molecular weight of 120,227, consists of an N-terminal signal peptide, a cellulose-binding domain of family III, and six successive cohesin domains. The molecular architecture of C. josui CipA is similar to those of the scaffolding proteins reported so far, such as Clostridium thermocellum CipA, Clostridium cellulovorans CbpA, and Clostridium cellulolyticum CipC, but C. josui CipA is considerably smaller than the other scaffolding proteins. CelD consists of an N-terminal signal peptide, a **family 48** catalytic domain of glycosyl hydrolase, and a dockerin domain. N-terminal amino acid sequence analysis of the C. josui cellulosomal proteins indicates that both CipA and CelD are major components of the cellulosome.

L14 ANSWER 10 OF 17 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 1998154434 MEDLINE
DOCUMENT NUMBER: 98154434 PubMed ID: 9493383
TITLE: Properties and gene structure of a bifunctional cellulolytic enzyme (CelA) from the extreme thermophile 'Anaerocellum thermophilum' with separate glycosyl hydrolase family 9 and 48 catalytic domains.
AUTHOR: Zverlov V; Mahr S; Riedel K; Bronnenmeier K
CORPORATE SOURCE: Institute of Molecular Genetics, Russian Academy of Science, Moscow, Russia.
SOURCE: MICROBIOLOGY, (1998 Feb) 144 (Pt 2) 457-65. Journal code: 9430468. ISSN: 1350-0872.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Z86105
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980430
Last Updated on STN: 19980430
Entered Medline: 19980421

AB A large cellulolytic enzyme (CelA) with the ability to hydrolyse microcrystalline cellulose was isolated from the extremely thermophilic, cellulolytic bacterium 'Anaerocellum thermophilum'. Full-length CelA and a truncated enzyme species designated CelA' were purified to homogeneity from culture supernatants. CelA has an apparent molecular mass of 230 kDa. The enzyme exhibited significant activity towards Avicel and was most active towards soluble substrates such as CM-cellulose (CMC) and beta-glucan. Maximal activity was observed between pH values of 5 and 6 and temperatures of 95 degrees C (CM-**cellulase**) and 85 degrees C (Avicelase). Cellobiose, glucose and minor amounts of cellotriose were

observed as end-products of Avicel degradation. The CelA-encoding gene was isolated from genomic DNA of 'A. thermophilum' by PCR and the nucleotide sequence was determined. The celA gene encodes a protein of 1711 amino acids (190 kDa) starting with the sequence found at the N-terminus of CelA purified from 'A. thermophilum'. Sequence analysis revealed a multidomain structure consisting of two distinct catalytic domains homologous to glycosyl hydrolase families 9 and 48 and three domains homologous to family III cellulose-binding domain linked by Pro-Thr-Ser-rich regions. The enzyme is most closely related to CelA of Caldicellulosiruptor saccharolyticus (sequence identities of 96 and 97% were found for the N- and C-terminal catalytic domains, respectively). Endoglucanase CelZ of Clostridium stercorarium shows 70.4% sequence identity to the N-terminal family 9 domain and exoglucanase CelY from the same organism has 69.2% amino acid identity with the C-terminal **family 48** domain. Consistent with this similarity on the primary structure level, the 90 kDa truncated derivative CelA' containing the N-terminal half of CelA exhibited endoglucanase activity and bound to microcrystalline cellulose. Due to the significantly enhanced Avicelase activity of full-length CelA, exoglucanase activity may be ascribed to the C-terminal **family 48** catalytic domain.

L14 ANSWER 11 OF 17 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 1998437496 MEDLINE
DOCUMENT NUMBER: 98437496 PubMed ID: 9761829
TITLE: Crystallization of the catalytic domain of Clostridium cellulolyticum CeLF **cellulase** in the presence of a newly synthesized **cellulase** inhibitor.
AUTHOR: Reverbel-Leroy C; Parsiegla G; Moreau V; Juy M; Tardif C; Driguez H; Belaich J P; Haser R
CORPORATE SOURCE: Universite de Provence, Place Victor-Hugo, 13331 Marseille CEDEX 3, France.
SOURCE: ACTA CRYSTALLOGRAPHICA. SECTION D: BIOLOGICAL CRYSTALLOGRAPHY, (1998 Jan 1) 54 (Pt 1) 114-8. Journal code: 9305878. ISSN: 0907-4449.
PUB. COUNTRY: Denmark
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981130
AB The catalytic domain of the CeIF processive endocellulase, a **family 48** glycosyl hydrolase from Clostridium cellulolyticum has been crystallized in the presence of a newly synthesized inhibitor (methyl 4-S-beta-cellobiosyl-4-thio-beta-cellobioside), by vapour diffusion, using PEG as a precipitant. The protein crystallizes in the orthorhombic P212121 space group and diffracts to a resolution of 2.0 A. The unit-cell parameters are a = 61.4, b = 84.5, c = 121.9 A.

L14 ANSWER 12 OF 17 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 97237718 MEDLINE
DOCUMENT NUMBER: 97237718 PubMed ID: 9084173
TITLE: Structure of the Clostridium stercorarium gene celY encoding the exo-1,4-beta-glucanase Avicelase II.
AUTHOR: Bronnenmeier K; Kundt K; Riedel K; Schwarz W H; Staudenbauer W L
CORPORATE SOURCE: Institute for Microbiology, Technical University Munich, Eederal Republic of Germany.
SOURCE: MICROBIOLOGY, (1997 Mar) 143 (Pt 3) 891-8. Journal code: 9430468. ISSN: 1350-0872.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D16670; GENBANK-L06942; GENBANK-L32742; GENBANK-L38827; GENBANK-U30321; GENBANK-Z69359
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 19970609
Last Updated on STN: 19970609
Entered Medline: 19970529

AB The nucleotide sequence of the celY gene coding for the thermostable exo-1,4-beta-glucanase Avicelase II of Clostridium stercorarium was determined. The gene consists of an ORF of 274Z bp which encodes a preprotein of 914 amino acids with a molecular mass of 103 kDa. The signal-peptide cleavage site was identified by comparison with the N-terminal amino acid sequence of Avicelase II purified from C stercorarium. The celY gene is located in close vicinity to the celZ gene coding for the endo-1,4-beta-glucanase Avicelase I. The CelY-encoding sequence was isolated from genomic DNA of C. stercorarium with the PCR technique. The recombinant enzyme produced in Escherichia coli as a LacZ'-CelY fusion protein could be purified using a simple two-step procedure. The properties of CelY proved to be consistent with those of Avicelase II purified from C. stercorarium. Sequence comparison revealed that CelY consists of an N-terminal catalytic domain flanked by a domain of 95 amino acids with unknown function joined to a type III cellulose-binding domain. The catalytic domain belongs to the recently proposed family L of **cellulases** (**family 48** of glycosyl hydrolases).

L14 ANSWER 13 OF 17 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 97:742566 SCISEARCH
THE GENUINE ARTICLE: XZ128
TITLE: Attack of carboxymethylcellulose at opposite ends by two cellobiohydrolases from Cellulomonas fimi
AUTHOR: Gilkes N R (Reprint); Kwan E; Kilburn D G; Miller R C; Warren R A J
CORPORATE SOURCE: UNIV BRITISH COLUMBIA, DEPT MICROBIOL & IMMUNOL, 300-6174 UNIV BLVD, VANCOUVER, BC V6T 1Z3, CANADA (Reprint); UNIV BRITISH COLUMBIA, PROT ENGN NETWORK CTR EXCELLENCE, VANCOUVER, BC V6T 1Z3, CANADA
COUNTRY OF AUTHOR: CANADA
SOURCE: JOURNAL OF BIOTECHNOLOGY, (16 SEP 1997) Vol. 57, No. 1-3, pp. 83-90.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0168-1656.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI
LANGUAGE: English
REFERENCE COUNT: 30

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The patterns of reducing sugar release following sequential addition of two Cellulomonas fimi cellobiohydrolases to carboxymethylcellulose corroborate previous evidence for preferential attack of beta-1,4-glucans at opposite ends. In other experiments, sequential additions involving a single cellobiohydrolase and an Agrobacterium beta-glucosidase indicate that CbhA attacks preferentially from the non-reducing end, CbhB from the reducing end. We suggest that all aerobic bacteria and fungi involved in cellulose hydrolysis produce a similar pair of cellobiohydrolases: a family 6 cellobiohydrolase that attacks from the non-reducing end and a **family 48** (bacterial) or family 7 (fungal) cellobiohydrolase that attacks from the reducing end. (C) 1997 Elsevier Science B.V.

L14 ANSWER 14 OF 17 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 97090419 MEDLINE

DOCUMENT NUMBER: 97090419 PubMed ID: 8936327
TITLE: Molecular study and overexpression of the Clostridium cellulolyticum celF **cellulase** gene in Escherichia coli.
AUTHOR: Reverbel-Leroy C; Belaich A; Bernadac A; Gaudin C; Belaich J P; Tardif C
CORPORATE SOURCE: Bioenergetique et Ingenierie des proteines, Centre National de la Recherche Scientifique, Marseille, France.
SOURCE: MICROBIOLOGY, (1996 Apr) 142 (Pt 4) 1013-23.
Journal code: 9430468. ISSN: 1350-0872.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U30321
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 19980206
Entered Medline: 19961231

AB The CelF-encoding sequence was isolated from Clostridium cellulolyticum genomic DNA using the inverse PCR technique. The gene lies between cipC (the gene encoding the cellulosome scaffolding protein) and celC (coding for the endoglucanase C) in the large cel cluster of this mesophilic cellulolytic Clostridium species. Comparisons between the deduced amino acid sequence of the mature CelF (693 amino acids, molecular mass 77626) and those of other beta-glycanases showed that this enzyme belongs to the recently proposed family L of **cellulases** (**family 48** of glycosyl hydrolases). The protein was overproduced in Escherichia coli using the T7 expression system. It formed both cytoplasmic and periplasmic inclusion bodies when induction was performed at 37 degrees C. Surprisingly, the protein synthesized from the cytoplasmic production vector was degraded in the Ion protease-deficient strain BL21(DE3). The induction conditions were optimized with regard to the concentration of inductor, cell density, and temperature and time of induction in order to overproduce an active periplasmic protein (CelFp) which was both soluble and stable. It was collected using the osmotic shock method. The enzymic degradation of various cellulosic substrates by CelFp was studied. CelFp degraded swollen Avicel more efficiently than substituted soluble CM-cellulose or crystalline Avicel and was not active on xylan. Its activity is therefore quite different from that of endoglucanases, which are most active on CM-cellulose.

L14 ANSWER 15 OF 17 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:683734 CAPLUS
DOCUMENT NUMBER: 126:44206
TITLE: Similarities between bacterial and fungal **cellulase** systems
AUTHOR(S): Miller, R. C., Jr.; Gilkes, N. R.; Johnson, P.; Kilburn, D. G.; Kwan, E.; Meinke, A.; Schmuck, M.; Shen, H.; Tomme, P.; Warren, R. A. J.
CORPORATE SOURCE: Dept. Microbiol. Immunol., Univ. British Columbia, Vancouver, BC, V6T 1Z3, Can.
SOURCE: Biotechnology in the Pulp and Paper Industry: Recent Advances in Applied and Fundamental Research, Proceedings of the International Conference on Biotechnology in the Pulp and Paper Industry, 6th, Vienna, June 11-15, 1995 (1996), Meeting Date 1995, 531-536. Editor(s): Srebotnik, Ewald; Messner, Kurt. Facultas-Universitaetsverlag: Vienna, Austria.
CODEN: 63OUAN
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review with 28 refs. Six **cellulases** and two xylanases from the cellulolytic bacterium Cellulomonas fimi have now been characterized

in detail. All contain a catalytic domain and a cellulose-binding domain; in some, addnl. domains are present. The enzymes adopt extended conformations spanning ten or more cellobiosyl residues. This review is focused on two recently discovered C. fimi **cellulases**: CbhA and CbhB. The catalytic domain of CbhA is closely related to that of Trichoderma reesei CBH II in family 6 of the .beta.-1,4-glucanases. Biochem. analyses show that CbhA is an exocellobiohydrolase, like CBH II. By analogy to CBH II, CbhA attacks substrates from the non-reducing end. The second enzyme, CbhB, is also an exocellobiohydrolase. It is a member of a new family of bacterial .beta.-1,4-glucanases designated **family 48**. CbhB appears to attack substrates from the reducing end. We suggest that a pair of cellobiohydrolases, which attack opposite ends of cellulose mols., is a general feature of **cellulase** systems from aerobic bacteria and fungi.

L14 ANSWER 16 OF 17 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 96:111964 SCISEARCH
THE GENUINE ARTICLE: BE51K
TITLE: CELLULOMONAS-FIMI CELLOBIOHYDROLASES
AUTHOR: SHEN H; MEINKE A; TOMME P; DAMUDE H G; KWAN E; KILBURN D G; MILLER R C; WARREN R A J; GILKES N R (Reprint)
CORPORATE SOURCE: UNIV BRITISH COLUMBIA, DEPT MICROBIOL & IMMUNOL, 300-6174 UNIV BLVD, VANCOUVER, BC V6T 1Z3, CANADA (Reprint); UNIV BRITISH COLUMBIA, DEPT MICROBIOL & IMMUNOL, VANCOUVER, BC V6T 1Z3, CANADA
COUNTRY OF AUTHOR: CANADA
SOURCE: ACS SYMPOSIUM SERIES, (1995) Vol. 618, pp. 174-196. ISSN: 0097-6156.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: ENGLISH
REFERENCE COUNT: 66
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The cellulolytic bacterium Cellulomonas fimi produces two cellobiohydrolases, CbhA and CbhB. These enzymes are major extracellular components during growth on cellulose. They correspond to previously identified cellulose-binding proteins, cbp95 and cbp120, respectively. Both comprise an N-terminal catalytic domain joined to three fibronectin type III modules and a C-terminal cellulose-binding domain. Amino acid sequence comparison shows that the CbhA catalytic domain is closely related to the catalytic domains of Trichoderma reesei CBH II and other fungal cellobiohydrolases in beta-1,4-glucanase family B. CbhB is a member of a new beta-1,4-glucanase family, designated family L (also called **family 48**). On the basis of data for CbhB, hydrolysis by family L enzymes proceeds with inversion of configuration at the anomeric carbon. CbhA and CbhB produce cellobiose from cellulose. Viscometric analysis of carboxymethylcellulose hydrolysis shows that both enzymes are predominantly exohydrolytic but Congo Red staining shows they also have weak endoglucanase activity. CbhB attacks cellohexaose from the reducing end. We suggest that C. fimi and T. reesei use similar strategies to hydrolyze cellulose because both appear to produce two types of cellobiohydrolase: one that attacks cellulose from the reducing end and another that attacks from the non-reducing end.

L14 ANSWER 17 OF 17 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 96003898 MEDLINE
DOCUMENT NUMBER: 96003898 PubMed ID: 7575482
TITLE: Cellobiohydrolase B, a second exo-cellobiohydrolase from the cellulolytic bacterium Cellulomonas fimi.
AUTHOR: Shen H; Gilkes N R; Kilburn D G; Miller R C Jr; Warren R A
CORPORATE SOURCE: Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.
SOURCE: BIOCHEMICAL JOURNAL, (1995 Oct 1) 311 (Pt 1) 67-74. Journal code: 2984726R. ISSN: 0264-6021.
PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D16670; GENBANK-L06942; GENBANK-L32742; GENBANK-L38827; GENBANK-M87018
ENTRY MONTH: 199511
ENTRY DATE: Entered STN: 19951227
Last Updated on STN: 19951227
Entered Medline: 19951109

AB The gene cbhB from the cellulolytic bacterium Cellulomonas fimi encodes a polypeptide of 1090 amino acids. Cellobiohydrolase B (CbhB) is 1037 amino acids long, with a calculated molecular mass of 109765 Da. The enzyme comprises five domains: an N-terminal catalytic domain of 643 amino acids, three fibronectin type III repeats of 97 amino acids each, and a C-terminal cellulose-binding domain of 104 amino acids. The catalytic domain belongs to **family 48** of glycosyl hydrolases.
CbhB has a very low activity on CM-cellulose. Viscometric analysis of CM-cellulose hydrolysis indicates that the enzyme is an exoglucanase. Cellobiose is the major product of hydrolysis of cellulose. In common with two other exoglycanases from C. fimi, CbhB has low but detectable endoglucanase activity. CbhB is the second exo-cellobiohydrolase found in C. fimi. Therefore, the **cellulase** system of C. fimi resembles those of fungi in comprising multiple endoglucanases and cellobiohydrolases.